ENTERED   OIPE

RAW SEQUENCE LISTING   DATE: 03/11/2002
PATENT APPLICATION: US/10/081,408   TIME: 10:21:47

Input Set : **A:\Ep.txt**
Output Set: **N:\CRF3\03112002\J081408.raw**

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 4 <110> APPLICANT: Abrahms,n , Lars
 5         Nilsson, Joakim
 7 <120> TITLE OF INVENTION: METHODS FOR PROTEIN PURIFICATION
10 <130> FILE REFERENCE: 13425-053001
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C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/081,408
C--> 12 <141> CURRENT FILING DATE: 2002-02-21
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12 <150> PRIOR APPLICATION NUMBER: SE 0100625-3
13 <151> PRIOR FILING DATE: 2001-02-23
15 <150> PRIOR APPLICATION NUMBER: US 60/272,247
16 <151> PRIOR FILING DATE: 2001-02-28
18 <160> NUMBER OF SEQ ID NOS: 20
20 <170> SOFTWARE: FastSEQ for Windows Version 4.0
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 4040
24 <212> TYPE: DNA
25 <213> ORGANISM: Homo sapiens
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (161)...(2449)
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33 gccccccacc ccgtccagga gccaacagag cccccgtctt gctggcgtga gaatacattg      120
34 ctctcctttg gttgaatcag ctgtccctct tcgtgggaaa atg aac cag aag aca        175
35                                                 Met Asn Gln Lys Thr
36                                                  1               5
38 atc ctc gtg ctc ctc att ctg gcc gtc atc acc atc ttt gcc ttg gtt       223
39 Ile Leu Val Leu Leu Ile Leu Ala Val Ile Thr Ile Phe Ala Leu Val
40               10              15              20
42 tgt gtc ctg ctg gtg ggc agg ggt gga gat ggg ggt gaa ccc agc cag      271
43 Cys Val Leu Leu Val Gly Arg Gly Gly Asp Gly Gly Glu Pro Ser Gln
44           25              30              35
46 ctt ccc cat tgc ccc tct gta tct ccc agt gcc cag cct tgg aca cac      319
47 Leu Pro His Cys Pro Ser Val Ser Pro Ser Ala Gln Pro Trp Thr His
48           40              45              50
50 cct ggc cag agc cag ctg ttt gca gac ctg agc cga gag gag ctg acg      367
51 Pro Gly Gln Ser Gln Leu Phe Ala Asp Leu Ser Arg Glu Glu Leu Thr
52       55              60              65
54 gct gtg atg cgc ttt ctg acc cag cgg ctg ggg cca ggg ctg gtg gat      415
55 Ala Val Met Arg Phe Leu Thr Gln Arg Leu Gly Pro Gly Leu Val Asp
56  70              75              80              85
58 gca gcc cag gcc cgg ccc tcg gac aac tgt gtc ttc tca gtg gag ttg      463
59 Ala Ala Gln Ala Arg Pro Ser Asp Asn Cys Val Phe Ser Val Glu Leu
60           90              95              100
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```
62 cag ctg cct ccc aag gct gca gcc ctg gct cac ttg gac agg ggg agc    511
63 Gln Leu Pro Pro Lys Ala Ala Ala Leu Ala His Leu Asp Arg Gly Ser
64         105                 110                 115
66 ccc cca cct gcc cgg gag gca ctg gcc atc gtc ttc ttt ggc agg caa    559
67 Pro Pro Pro Ala Arg Glu Ala Leu Ala Ile Val Phe Phe Gly Arg Gln
68         120                 125                 130
70 ccc cag ccc aac gtg agt gag ctg gtg gtg ggg cca ctg cct cac ccc    607
71 Pro Gln Pro Asn Val Ser Glu Leu Val Val Gly Pro Leu Pro His Pro
72         135                 140                 145
74 tcc tac atg cgg gac gtg act gtg gag cgt cat gga ggc ccc ctg ccc    655
75 Ser Tyr Met Arg Asp Val Thr Val Glu Arg His Gly Gly Pro Leu Pro
76 150                 155                 160                 165
78 tat cac cga cgc ccc gtg ctg ttc caa gag tac ctg gac ata gac cag    703
79 Tyr His Arg Arg Pro Val Leu Phe Gln Glu Tyr Leu Asp Ile Asp Gln
80         170                 175                 180
82 atg atc ttc aac aga gag ctg ccc cag gct tct ggg ctt ctc cac cac    751
83 Met Ile Phe Asn Arg Glu Leu Pro Gln Ala Ser Gly Leu Leu His His
84         185                 190                 195
86 tgt tgc ttc tac aag cac cgg gga cgg aac ctg gtg aca atg acc acg    799
87 Cys Cys Phe Tyr Lys His Arg Gly Arg Asn Leu Val Thr Met Thr Thr
88         200                 205                 210
90 gct ccc cgt ggt ctg caa tca ggg gac cgg gcc acc tgg ttt ggc ctc    847
91 Ala Pro Arg Gly Leu Gln Ser Gly Asp Arg Ala Thr Trp Phe Gly Leu
92         215                 220                 225
94 tac tac aac atc tcg ggc gct ggg ttc ttc ctg cac cac gtg ggc ttg    895
95 Tyr Tyr Asn Ile Ser Gly Ala Gly Phe Phe Leu His His Val Gly Leu
96 230                 235                 240                 245
98 gag ctg cta gtg aac cac aag gcc ctt gac cct gcc cgc tgg act atc    943
99 Glu Leu Leu Val Asn His Lys Ala Leu Asp Pro Ala Arg Trp Thr Ile
100                 250                 255                 260
102 cag aag gtg ttc tat caa ggc cgc tac tac gac agc ctg gcc cag ctg    991
103 Gln Lys Val Phe Tyr Gln Gly Arg Tyr Tyr Asp Ser Leu Ala Gln Leu
104                 265                 270                 275
106 gag gcc cag ttt gag gcc ggc ctg gtg aat gtg gtg ctg atc cca gac    1039
107 Glu Ala Gln Phe Glu Ala Gly Leu Val Asn Val Val Leu Ile Pro Asp
108         280                 285                 290
110 aat ggc aca ggt ggg tcc tgg tcc ctg aag tcc cct gtg ccc ccg ggt    1087
111 Asn Gly Thr Gly Gly Ser Trp Ser Leu Lys Ser Pro Val Pro Pro Gly
112         295                 300                 305
114 cca gct ccc cct cta cag ttc tat ccc caa ggc ccc cgc ttc agt gtc    1135
115 Pro Ala Pro Pro Leu Gln Phe Tyr Pro Gln Gly Pro Arg Phe Ser Val
116 310                 315                 320                 325
118 cag gga agt cga gtg gcc tcc tca ctg tgg act ttc tcc ttt ggc ctc    1183
119 Gln Gly Ser Arg Val Ala Ser Ser Leu Trp Thr Phe Ser Phe Gly Leu
120         330                 335                 340
122 gga gca ttc agt ggc cca agg atc ttt gac gtt cgc ttc caa gga gaa    1231
123 Gly Ala Phe Ser Gly Pro Arg Ile Phe Asp Val Arg Phe Gln Gly Glu
124         345                 350                 355
126 aga cta gtt tat gag ata agc ctc caa gag gcc ttg gcc atc tat ggt    1279
```

```
127 Arg Leu Val Tyr Glu Ile Ser Leu Gln Glu Ala Leu Ala Ile Tyr Gly
128         360                 365                 370
130 gga aat tcc cca gca gca atg acg acc cgc tat gtg gat gga ggc ttt   1327
131 Gly Asn Ser Pro Ala Ala Met Thr Thr Arg Tyr Val Asp Gly Gly Phe
132     375                 380                 385
134 ggc atg ggc aag tac acc acg ccc ctg acc cgt ggg gtg gac tgc ccc   1375
135 Gly Met Gly Lys Tyr Thr Thr Pro Leu Thr Arg Gly Val Asp Cys Pro
136 390                 395                 400                 405
138 tac ttg gcc acc tac gtg gac tgg cac ttc ctt ttg gag tcc cag gcc   1423
139 Tyr Leu Ala Thr Tyr Val Asp Trp His Phe Leu Leu Glu Ser Gln Ala
140                 410                 415                 420
142 ccc aag aca ata cgt gat gcc ttt tgt gtg ttt gaa cag aac cag ggc   1471
143 Pro Lys Thr Ile Arg Asp Ala Phe Cys Val Phe Glu Gln Asn Gln Gly
144             425                 430                 435
146 ctc ccc ctg cgg cga cac cac tca gat ctc tac tcg cac tac ttt ggg   1519
147 Leu Pro Leu Arg Arg His His Ser Asp Leu Tyr Ser His Tyr Phe Gly
148         440                 445                 450
150 ggt ctt gcg gaa acg gtg ctg gtc gtc aga tct atg tcc acc ttg ctc   1567
151 Gly Leu Ala Glu Thr Val Leu Val Val Arg Ser Met Ser Thr Leu Leu
152     455                 460                 465
154 aac tat gac tat gtg tgg gat acg gtc ttc cac ccc agt ggg gcc ata   1615
155 Asn Tyr Asp Tyr Val Trp Asp Thr Val Phe His Pro Ser Gly Ala Ile
156 470                 475                 480                 485
158 gaa ata cga ttc tat gcc acg ggc tac atc agc tcg gca ttc ctc ttt   1663
159 Glu Ile Arg Phe Tyr Ala Thr Gly Tyr Ile Ser Ser Ala Phe Leu Phe
160                 490                 495                 500
162 ggt gct act ggg aag tac ggg aac caa gtg tca gag cac acc ctg ggc   1711
163 Gly Ala Thr Gly Lys Tyr Gly Asn Gln Val Ser Glu His Thr Leu Gly
164             505                 510                 515
166 acg gtc cac acc cac agc gcc cac ttc aag gtg gat ctg gat gta gca   1759
167 Thr Val His Thr His Ser Ala His Phe Lys Val Asp Leu Asp Val Ala
168         520                 525                 530
170 gga ctg gag aac tgg gtc tgg gcc gag gat atg gtc ttt gtc ccc atg   1807
171 Gly Leu Glu Asn Trp Val Trp Ala Glu Asp Met Val Phe Val Pro Met
172     535                 540                 545
174 gct gtg ccc tgg agc cct gag cac cag ctg cag agg ctg cag gtg acc   1855
175 Ala Val Pro Trp Ser Pro Glu His Gln Leu Gln Arg Leu Gln Val Thr
176 550                 555                 560                 565
178 cgg aag ctg ctg gag atg gag gag cag gcc gcc ttc ctc gtg gga agc   1903
179 Arg Lys Leu Leu Glu Met Glu Glu Gln Ala Ala Phe Leu Val Gly Ser
180                 570                 575                 580
182 gcc acc cct cgc tac ctg tac ctg gcc agc aac cac agc aac aag tgg   1951
183 Ala Thr Pro Arg Tyr Leu Tyr Leu Ala Ser Asn His Ser Asn Lys Trp
184             585                 590                 595
186 ggt cac ccc cgg ggc tac cgc atc cag atg ctc agc ttt gct gga gag   1999
187 Gly His Pro Arg Gly Tyr Arg Ile Gln Met Leu Ser Phe Ala Gly Glu
188         600                 605                 610
190 ccg ctg ccc caa aac agc tcc atg gcg aga ggc ttc agc tgg gag agg   2047
191 Pro Leu Pro Gln Asn Ser Ser Met Ala Arg Gly Phe Ser Trp Glu Arg
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192     615                   620                   625
194 tac cag ctg gct gtg acc cag cgg aag gag gag gag ccc agt agc agc    2095
195 Tyr Gln Leu Ala Val Thr Gln Arg Lys Glu Glu Glu Pro Ser Ser Ser
196 630                   635                   640                   645
198 agc gtt ttc aat cag aat gac cct tgg gcc ccc act gtg gat ttc agt    2143
199 Ser Val Phe Asn Gln Asn Asp Pro Trp Ala Pro Thr Val Asp Phe Ser
200                   650                   655                   660
202 gac ttc atc aac aat gag acc att gct gga aag gat ttg gtg gcc tgg    2191
203 Asp Phe Ile Asn Asn Glu Thr Ile Ala Gly Lys Asp Leu Val Ala Trp
204                   665                   670                   675
206 gtg aca gct ggt ttt ctg cat atc cca cat gca gag gac att cct aac    2239
207 Val Thr Ala Gly Phe Leu His Ile Pro His Ala Glu Asp Ile Pro Asn
208         680                   685                   690
210 aca gtg act gtg ggg aac ggc gtg ggc ttc ttc ctc cga ccc tat aac    2287
211 Thr Val Thr Val Gly Asn Gly Val Gly Phe Phe Leu Arg Pro Tyr Asn
212     695                   700                   705
214 ttc ttt gac gaa gac ccc tcc ttc tac tct gcc gac tcc atc tac ttc    2335
215 Phe Phe Asp Glu Asp Pro Ser Phe Tyr Ser Ala Asp Ser Ile Tyr Phe
216 710                   715                   720                   725
218 cga ggg gac cag gat gct ggg gcc tgc gag gtc aac ccc cta gct tgc    2383
219 Arg Gly Asp Gln Asp Ala Gly Ala Cys Glu Val Asn Pro Leu Ala Cys
220                   730                   735                   740
222 ctg ccc cag gct gct gcc tgt gcc ccc gac ctc cct gcc ttc tcc cac    2431
223 Leu Pro Gln Ala Ala Ala Cys Ala Pro Asp Leu Pro Ala Phe Ser His
224         745                   750                   755
226 ggg ggc ttc tct cac aac taggcggtcc tgggatgggg catgtggcca           2479
227 Gly Gly Phe Ser His Asn
228         760
230 agggctccag ggccagggtg tgagggatgg ggagcagctg ggcactgggc cggcagcctg   2539
231 gttccctctt tcctgtgcca ggactctctt tcttccacta ccctccctcg catccgcctc   2599
232 tgagccagga gcctcctgac cctgtgatgc ctgacacagg ggacactgaa ccttgttgat   2659
233 gccagctgta ctgagttctc atccacagag gccaggcatg gcccagcctg gagccgtggc   2719
234 cgagggcttc cctagatggt tccctttgtt gctgtctggc tttcccgaat ctttttaggc   2779
235 cacctccaag gactctaaaa gggggctatt ccctggagac cccagagtag ggttgccagt   2839
236 cctgcaagtc catagctgag ctggaaagga tgcttctgct cacattccct ctcatccagg   2899
237 tcctttcctt ctcgtcttcc tctctctcac ctacttcctc ctcctcctcc tgttcctgcc   2959
238 ttctcttcta tcctgcaatt tctcccgaat cctgaggga tatccctatg tcccagcccc    3019
239 tggtactccc ccagccctca gttttcagtc aagttccgtc tcctctccag ccctatggaa   3079
240 gtctcaaggt cacgggaccc ctaatcagag tggccaatcc ctgtgtgtcg ttcccttgtg   3139
241 tctgttgctt attgggagta ggagttgctc ctacccctgt cctggggctg ggtgtgtttc   3199
242 aggacagctg cttctgtgca tttgtgtctg cctgcctcat gctctctata gaggaggatg   3259
243 gtcatcgtga cagcagcagc tcaagttagc atttcaagtg atttgggggt gcaatgataa   3319
244 tgaagaatgg ccattttgta ccagggctct gtattctgca acagcctgtt tgggaggctg   3379
245 gagtggaaac aaagggtggg catcaaagat gagaagccaa agcccctaca actccagcca   3439
246 cccagccagg aggggctgtc caatcacatt caggcatgcg aatgagctgg ccctgggtg    3499
247 aggtgggggt ctggcctagt ggggaggggc ctggcctggg tggggcaggg cctggcctgg   3559
248 tccaggcttg ggctccattc ccatcactgc tgtccctcct gaggtctgga ttggggatgg   3619
249 ggacaaagaa atagcaagag atgagaaaca acagaaactt ttttctctaa aggactggtt   3679
250 aaatcaattc tgatacagcc ttacaataca atagtatgca gctaaaaaat aattgtatgt   3739
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RAW SEQUENCE LISTING   DATE: 03/11/2002
PATENT APPLICATION: US/10/081,408   TIME: 10:21:47

Input Set : A:\Ep.txt
Output Set: N:\CRF3\03112002\J081408.raw

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251 ctttatatac taatatgtaa taatcttcag gtgaaaaagg caagccacag aaatgtgtat  3799
252 agcgcacttc ccatttgtgt ttcagaaagg agtagaatat aaacacataa ttgcttatgt  3859
253 atgcctattc agaataaatg'ggtaacactg attacttttg ggaggggaac cagtaggttg  3919
254 aggacaggag agggaagggt cttaacactt acaccctttt gtacattttg aattttgaac  3979
255 catgtgactg tattacctat tcaaaataaa caataaatgg gcccaaaaaa aaaaaaaaaa  4039
256 a                                                                   4040
258 <210> SEQ ID NO: 2
259 <211> LENGTH: 763
260 <212> TYPE: PRT
261 <213> ORGANISM: Homo sapiens
263 <400> SEQUENCE: 2
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265 1               5                   10                  15
266 Ile Phe Ala Leu Val Cys Val Leu Leu Val Gly Arg Gly Gly Asp Gly
267             20                  25                  30
268 Gly Glu Pro Ser Gln Leu Pro His Cys Pro Ser Val Ser Pro Ser Ala
269         35                  40                  45
270 Gln Pro Trp Thr His Pro Gly Gln Ser Gln Leu Phe Ala Asp Leu Ser
271     50                  55                  60
272 Arg Glu Glu Leu Thr Ala Val Met Arg Phe Leu Thr Gln Arg Leu Gly
273 65                  70                  75                  80
274 Pro Gly Leu Val Asp Ala Ala Gln Ala Arg Pro Ser Asp Asn Cys Val
275                 85                  90                  95
276 Phe Ser Val Glu Leu Gln Leu Pro Pro Lys Ala Ala Ala Leu Ala His
277             100                 105                 110
278 Leu Asp Arg Gly Ser Pro Pro Pro Ala Arg Glu Ala Leu Ala Ile Val
279         115                 120                 125
280 Phe Phe Gly Arg Gln Pro Gln Pro Asn Val Ser Glu Leu Val Val Gly
281     130                 135                 140
282 Pro Leu Pro His Pro Ser Tyr Met Arg Asp Val Thr Val Glu Arg His
283 145                 150                 155                 160
284 Gly Gly Pro Leu Pro Tyr His Arg Arg Pro Val Leu Phe Gln Glu Tyr
285                 165                 170                 175
286 Leu Asp Ile Asp Gln Met Ile Phe Asn Arg Glu Leu Pro Gln Ala Ser
287             180                 185                 190
288 Gly Leu Leu His His Cys Cys Phe Tyr Lys His Arg Gly Arg Asn Leu
289         195                 200                 205
290 Val Thr Met Thr Thr Ala Pro Arg Gly Leu Gln Ser Gly Asp Arg Ala
291     210                 215                 220
292 Thr Trp Phe Gly Leu Tyr Tyr Asn Ile Ser Gly Ala Gly Phe Phe Leu
293 225                 230                 235                 240
294 His His Val Gly Leu Glu Leu Leu Val Asn His Lys Ala Leu Asp Pro
295                 245                 250                 255
296 Ala Arg Trp Thr Ile Gln Lys Val Phe Tyr Gln Gly Arg Tyr Tyr Asp
297             260                 265                 270
298 Ser Leu Ala Gln Leu Glu Ala Gln Phe Glu Ala Gly Leu Val Asn Val
299         275                 280                 285
300 Val Leu Ile Pro Asp Asn Gly Thr Gly Gly Ser Trp Ser Leu Lys Ser
301     290                 295                 300
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Use of n and / or Xaa has been detected in the
Sequence Listing. Review the Sequence Listing
→ to ensure a corresponding explanation is present
in the <220> to <223> fields of each sequence
using n or Xaa.

VERIFICATION SUMMARY   DATE: 03/11/2002
PATENT APPLICATION: **US/10/081,408**   TIME: 10:21:48

Input Set : **A:\Ep.txt**
Output Set: **N:\CRF3\03112002\J081408.raw**

L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date